Circular RNA profile in gliomas revealed by identification tool UROBORUS.

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Public Summary:
We have developed a computational pipeline named UROBORUS with the goal of identifying genome-wide circular RNA (circRNA) based on total RNA-sequencing data.

Scientific Abstract:
Recent evidence suggests that many endogenous circular RNAs (circRNAs) may play roles in biological processes. However, the expression patterns and functions of circRNAs in human diseases are not well understood. Computationally identifying circRNAs from total RNA-seq data is a primary step in studying their expression pattern and biological roles. In this work, we have developed a computational pipeline named UROBORUS to detect circRNAs in total RNA-seq data. By applying UROBORUS to RNA-seq data from 46 gliomas and normal brain samples, we detected thousands of circRNAs supported by at least two read counts, followed by successful experimental validation on 24 circRNAs from the randomly selected 27 circRNAs. UROBORUS is an efficient tool that can detect circRNAs with low expression levels in total RNA-seq without RNase R treatment. The circRNAs expression profiling revealed more than 476 circular RNAs differentially expressed in control brain tissues and gliomas. Together with parental gene expression, we found that circRNA and its parental gene have diversified expression patterns in gliomas and control brain tissues. This study establishes an efficient and sensitive approach for predicting circRNAs using total RNA-seq data. The UROBORUS pipeline can be accessed freely for non-commercial purposes at http://uroborus.openbioinformatics.org/.

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